

Application No.: 10/506,670
Inventor: LIPKA
Reply to Office Action of Nov. 19, 2007
Docket No.: G1309 US S3

REMARKS/ARGUMENTS

Sequence Listing

The Examiner asserted that “[t]he sequences on Figs. 9 and 12 lack SEQ ID NO: Applicant is respectfully requested to identify the sequences on Figs. 9 and 12 or to submit a new Sequence Listing, which comprises said sequences.”

Applicant respectfully submits that 37 CFR § 1.1821(d) only requires the use of sequence identifiers in association with the written description and claims. The requirement does not extend to the drawing figures. Indeed, in the instant case, the addition of such identifiers would be wholly inappropriate in the context of the figures.

Amendments to the Specification

Applicant has amended the specification to include section headings as noted by the Examiner. With regard to the possible introduction of new matter by the use of url’s to describe websites, Applicant has amended the specification to indicate the state of such urls’ at the time of the instant application. Furthermore, Applicant respectfully submits that such url’s merely describe the state of the art at the time of the invention.

Amendments to the Drawings

Applicant has provided Replacement Drawing Sheets, which obviate the Examiner’s objections regarding the blurriness and darkness of the original figures.

Claim Amendments

1. Applicant has amended Claim 1 to replace “polynucleotides” with “a polynucleotide” as suggested by the Examiner.
2. Applicant has amended Claim 1 to replace “sequence identity of at least 50%,” with “sequence identity of at least 95%.” Support for the claim amendment can be found at least at page 10, paragraphs 2 and 3 of the original specification.

Application No.: 10/506,670
Inventor: LIPKA
Reply to Office Action of Nov. 19, 2007
Docket No.: G1309 US S3

3. Applicant has amended claim 1 to further recite “and said promoter providing a static defense and/or being inducible upon pathogen attack.” Support for the claim amendment can be found at least at page 4, lines 30-31, page 8, lines 17-20 and page 24, lines 12-14.

4. Applicant has added new claim 27, dependent from claim 1, and further reciting that “the promoter is active in the epidermis or the rhizodermis.” Support for new claim 27 can be found at least at page 23, lines 8-13 of the original specification.

5. Applicant has added new claim 28, dependent from claim 1, which further recites that the “promoter ensures expression in photosynthetically active tissues only.” Support for new claim 28 can be found at least at page 23, lines 14-20 of the original specification.

6. Applicant has amended claim 3 to recite “a vector comprising the recombinant nucleic acid molecule of claim 1.”

7. Applicant has amended other of the claims to address grammatical type issues and/or antecedent issues.

Claim Rejections under 35 USC § 112, second paragraph

The Examiner rejected claims 3-7 and 12-16 as allegedly indefinite. While not agreeing with the Examiner’s underlying basis for the rejection, Applicant has nonetheless, amended such claims to advance prosecution.

The rejections should be withdrawn.

Claim Rejections under 35 USC § 112, first paragraph

Claims 1-8 and 11-16 stand rejected as allegedly not reasonably enabling “a recombinant nucleic acid molecule comprising a polynucleotide encoding a fragment of SEQ ID NO: 2 or

Application No.: 10/506,670
Inventor: LIPKA
Reply to Office Action of Nov. 19, 2007
Docket No.: G1309 US S3

encoding a polypeptide having at least 50% [identity] to SEQ ID NO:2 and having beta-glucosidase activity.”

Applicant has amended claim 1 to delete element “(c)” and had further amended the claim to replace 50% with 95% thereby obviating the rejection. Applicant respectfully submits that in view of the state of the art and the instant disclosure, an ordinarily skilled artisan would be sufficiently enable to make make and use the claimed invention without undue experimentation.

The rejection should be withdrawn.

Claim Rejections under 35 USC § 102

1.) The Examiner rejected Claims 1-8 and 11-16 under 35 USC § 102(e) as allegedly being anticipated by Harper (US 7,109,033). More specifically, the Examiner asserted, “Harper teaches a recombinant nucleic acid/vector comprising a nucleotide sequence encoding a polypeptide that is 100% identical to Applicant's SEQ ID NO: 2 (see attached alignment of sequence) and having beta-glucosidase activity (see SEQ ID NO: 54 on Table 1; column 61) operably linked to regulatory sequences including a promoter region; transgenic plant/cell and host cells transformed with said vector or recombinant nucleic acid; and a method of transforming host cell/plant with said vector to produce transgenic plant having resistance against stress (see at least col. 4-5; paragraph bridging 13-14; col. 19-20, 29-34, and 43-49). Since the nucleic acid of Harper (SEQ ID NO: 54) is 100% identical to Applicant's SEQ ID NO: 1, the disease resistance activity is an inherent property to the Harper's SEQ ID NO: 54. Therefore, Harper teaches all claim limitations.”

Applicant has amended claim 1 to recite “a promoter operatively linked to said polynucleotide, said promoter being heterologous with respect to the polynucleotide and said promoter providing a static defense and/or being inducible upon pathogen attack,” and respectfully submits that Harper fails to explicitly or implicitly describe such features.

That is, Harper describes plant genes that are regulated in response to one or more abiotic stress conditions (See column 17, lines 4-5). As described at Col. 18, line 35 – Col. 19, line 3,

Application No.: 10/506,670
Inventor: LIPKA
Reply to Office Action of Nov. 19, 2007
Docket No.: G1309 US S3

abiotic stressors are defined as stressors of the type, for example, resulting from salt stress, drought stress, etc. Accordingly, Harper does not describe biotic stress and does not describe biotic stress caused by pathogens, and the like. More particularly, Harper does not describe promoters that provide static defense or inducible defense upon attack by pathogens. Accordingly, Harper fails to describe each and every element of amended claim 1 as is needed to support a rejection under 35 USC § 102.

The rejection should be withdrawn.

2.) The Examiner rejected Claims 1-8 and 11-16 under 35 USC 102(e) as allegedly anticipated by Duvick et al (US 6,433,249). More specifically, the Examiner asserted that Duvick describe an isolated gene encoding a polypeptide having beta glucosidase activity that is cloned into a plant expression vector comprising regulatory sequences, and methods of transforming a host cell and plants with said vector to produce transgenic plants having enhanced resistance to diseases and insects. The cited reference also teaches transformed plants and host cells expressing said polypeptide having beta glucosidase activity . Given that claim 1, part c encompasses "a fragment" of any size of SEQ ID NO: 2 having beta-glucosidase activity . Duvick et al discloses all claim limitations."

Applicant has amended claim 1 to delete "part (c)" and has further amended such claim to recite that the promoter is "operatively linked to said polynucleotide, said promoter being heterologous with respect to the polynucleotide and said promoter providing a static defense and/or being inducible upon pathogen attack," and respectfully submits that Duvick fails to explicitly or implicitly describe such features. Additionally, amended claim 1 further recites "a polynucleotide comprising a nucleotide sequence which encodes a polypeptide having a sequence identity of at least 95% to an amino acid sequence encoded by the polynucleotide of (a) or (b), wherein said polypeptide has R-glucosidase activity." However, as shown in Applicant's Appendix, results of GAP and BestFit sequence alignments of SEQ ID NO:1 of the claimed invention and SEQ ID NOS: 1 and 3 of Duvick set forth that there is less than 57% identity between the sequences. Similarly, the sequence alignment of SEQ ID NO: 2 of the claimed

Application No.: 10/506,670
Inventor: LIPKA
Reply to Office Action of Nov. 19, 2007
Docket No.: G1309 US S3


invention and SEQ ID NOS: 2 and 4 of Duvick illustrate an identity of below 50%. Accordingly, Applicant respectfully submits that Duvick further fails to disclose each and every element of amended claim 1 as required to support a rejection under 35 USC §102.

Accordingly, the rejection should be withdrawn.

Application No.: 10/506,670
Inventor: LIPKA
Reply to Office Action of Nov. 19, 2007
Docket No.: G1309 US S3

Conclusion

Applicants respectfully submit that the present application is in condition for allowance, which action is courteously requested. Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 14-1437. Please credit any excess fees to such deposit account.

Respectfully submitted,
NOVAK DRUCE & QUIGG, LLP

S. Peter Konzel
Registration No.: 53,152

Customer No.: 26474
1300 Eye St. N.W.
1000 West Tower
Washington, D.C. 20005
Phone: (202) 659-0100
Fax: (202) 659-0105

Dated: May 19, 2008

Application No.: 10/506,670
Inventor: LIPKA
Reply to Office Action of Nov. 19, 2007
Docket No.: G1309 US S3

APPENDIX

This appendix includes the following:

- 1.) Replacement Drawing Sheets; and,
- 2.) GAP (4) and BestFit (4) Sequence Alignment Comparisons.

attached Replacement Sheet and Annotated Sheet Showing Changes Made for consideration by the Examiner.

GAP (Present Application SEQ ID NO 1 versus Duvick SEQ ID NO 1)

GAP of: Present application from: 1 to: 1683

readseq-55023_tmp_1 1683 bp

to: DUVICK from: 1 to: 1931

readseq-53826_tmp_1 1931 bp

Symbol comparison table: /applications/gcg/share/matrix/nwsgapdna.cmp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 7929 Length: 1937
Ratio: 4.711 Gaps: 7
Percent Similarity: 50.030 Percent Identity: 50.030

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

. = 1

x May 16, 2008 19:06 ..

```

      .
      .
      .
1 .....atggcacatcttcaaagaacatttcctactgagatgtcaaaa 42
      | | | | | | | | | | | | | | | | | | | | |
201 gagtaggcagccaaaatggagtcctaatgttgagcccctcgaaatccca 250
      .
43 ggtagagctagctttccaaaaggctttctctttggaactgcttcatcttc 92
      | | | | | | | | | | | | | | | | | | | | |
251 caaagggactgggtccctctgacttcaccttcggtgccgccacttcagc 300
      .
93 ttatcagtagcgaaggagcagtgaatgaaggtgagaggacaaagcgtgt 142
      | | | | | | | | | | | | | | | | | | | | |
301 gtaccaaattgaaggtgcttgaatgaagatggaaaggggaaagcaact 350
      .
143 gggatcatttctccaacaggtttcctcacagaatcagtgattctagcgac 192
      | | | | | | | | | | | | | | | | | | | | |
351 gggatcacttctgccacaatcatccgaaaggatactggacgggagcaat 400
      .
193 ggaaacgttgccgttgatttctaccatcgttacaaggaagatattaagag 242
      | | | | | | | | | | | | | | | | | | | | |
401 tcagacattggagcgaattcgtatcatatgtacaaaacggacgtcagatt 450
      .
243 aatgaaggatataaacatggattcggttcggtttccattgcttggccac 292
      | | | | | | | | | | | | | | | | | | | | |
451 gctcaaggaaatgggcatggacgcataataggttctctatctcttggccca 500
      .
293 gagttctaccttatggcaaaagggatagaggagttagtgagaaggaatt 342
      | | | | | | | | | | | | | | | | | | | | |
501 gaatactgccgaagggaaccaaagaaggaggtattaaccctgatggcatc 550
      .
343 aagttttacaatgatgttattgatgaactcttagccaatgaaatcactcc 392
      | | | | | | | | | | | | | | | | | | | | |

```


551 aagtactacagaaacctcatcaacttgttgcctggaaaacggcatagagcc 600
393 tcttgttactatctttcattgggacataccacaggatcttgaagatgaat 442
||| || ||| ||| ||| ||||| ||||| ||| ||| ||||| |||
601 atatgtaacaattttccactgggatgtacctcaagcactagaagagaagt 650
443 acggcgggttttcta.....agcgagcagattatagatgacttcaga 483
||||||| || ||| ||| ||||| ||| |||
651 acggcggcttcttagataagagtcataagagcattgtagaagattacacc 700
484 gactatgcgagtcctctgcttcgagagatttggggacagagtgagtcctgtg 533
||| || | | ||||| || | || ||||| ||||| |||
701 tacttcgctaaggtgtgctttgataaacttcggcgacaaggtgaagaattg 750
534 gtgcacaatgaatgagccgtgggtctacagtgtcgcgggctatgacacag 583
|| | || | ||||| || | || | ||||| ||||| |||
751 gttgacctttaatgagccccagacatttacttccttttctacggaactg 800
584 gaaggaaagcgccaggacggtgctccaagtatgttaatggcgctagtgtt 633
| || ||||| ||||| ||| || | |||
801 gggctcttgccccaggctgggtgctcacctggactagactgtgcctaccga 850
634 gctggaatgtcgggatacagggcatatatattgtgagccataacatgcttct 683
|||| | || ||||| ||| || | || ||||| ||||| |||
851 actgggaattcactcgtcgagccttacactgctggccataacattctcct 900
684 agcgcacgcagaagcagtggaagtgttagaaaatgtgaccatattaaaa 733
||| ||||| || ||| ||||| || | || | ||| ||| |
901 agcccacgctgaggctgttgatctttacaacaagcattacaagcgcgacg 950
734 acggacaaattgggattgcgcataatccactttggtacgagccatatgat 783
|| | || ||||| || | || | || | ||||| |||
951 acaccgcgatagggcttgctttgacgtaatgggtcgtgtgccatacggga 1000
784 ccgagtgatccagatgatgtcgaaggatgtaatcgagctatggacttcat 833
| || ||||| || | || | || | ||||| |||
1001 acatcgtttctggataaacaggccgaa...gaaaggtcatgggacatcaa 1047
834 gcttgggttggcatcagcatccgactgcttgtggagactatccagaaacga 883
|| |||| | || | ||||| ||||| ||| |||
1048 cctaggatggttcttagagccagtggttcgtggtgactacccttctcca 1097
884 tgaagaaatcagttggagatagattaccgagttttacaccagaacaatct 933
||| || | ||||| ||||| || | |||||
1098 tgagatcattggctagggaaacgactacccttcttcaaggacgagcagaag 1147
934 aagaaacttataggctcttgcgattacgttgggtataaactactatagctc 983
|||| || || || | | || | ||||| ||||| |||
1148 gagaagctcgcgggttctataacatgttgggggttaactactacacctc 1197
984 gcttttcgtgaagagtatcaaacacgtggatcctacgcaacctacttgga 1033
| ||| || | ||| ||| |||||
1198 acggttctccaaaaacatcgacatctcaccaaaactactcacctgtgctca 1247
1034 gaactgaccaaggcggttgattggatgaaaaccaac...atagatgggaaa 1080
|||||| | || | || | || ||| || |||||
1248 aactgacgacgcctacgccagtcaagaagttaacgggcctgacgggaag 1297
1081 caaatagcaaaacaaggaggatcagagtgagtttcacatatccaacagg 1130
| || | | || ||||| ||||| ||| ||| |||
1298 cccattggtcctcctatgggaaatccatggatctacatgtaccctgaggg 1347
1131 actcagaaacattttgaagtatgtgaaaaaaacttatggcaatcctccca 1180

```

      | | | | | | | | | | | | | | | | | |
1348 cttgaaggatctccttatgataatgaagaacaaatacggaaacccaccta 1397
      .
1181 ttctcataactgaaaacgggtatggtgaagtagcggaacagagtcagagt 1230
      | | | | | | | | | | | | | | | | | |
1398 tctacatcaccgagaacggaatcggggatgttgataccaaagagacacct 1447
      .
1231 ctttatatgtacaatccttcaatcgacacagagagattggagtacattga 1280
      | | | | | | | | | | | | | | | | | |
1448 ctacccatggaggctgccttaaatactacaaaaggctagattacatcca 1497
      .
1281 aggcacatccacgctattcatcaagccatccatgaagatggagtaagag 1330
      | | | | | | | | | | | | | | | | | |
1498 gcgccacatcgctactcttaaggaatcaat...agacttgggatcaaatag 1544
      .
1331 tggaagggttattacgtatggtcattgctagataacttcgagtggaaacagt 1380
      | | | | | | | | | | | | | | | | | |
1545 tgcaaggctacttcgcttggctctgctggacaactttgaatggtttgcc 1594
      .
1381 ggatatggtgtgagatatggtttatattacattgattacaaagatgggct 1430
      | | | | | | | | | | | | | | | | | |
1595 ggcttcaccgaacggttatggcattgtctacgtcgaccgcaacaataactg 1644
      .
1431 tagacgatacccgaaaatgtcggcggttatggttgaaagagttcttga... 1477
      | | | | | | | | | | | | | | | | | |
1645 cacgcgctacatgaaggagtctgccaagtgggtgaaagagttcaacaccg 1694
      .
1478 ..ggtttgatcaagaagacgattcttcgac..gtctaagaaagaagagaa 1523
      | | | | | | | | | | | | | | | | | |
1695 cgaaaaagcccagcaagaagattcttacgccagcttaaaaatcgggggcc 1744
      .
1524 gaaagagagctatggaaaacagttattgcattctgttcaggacagtcaat 1573
      | | | | | | | | | | | | | | | | | |
1745 tcatgatgtgggtgcagcccataaaaacctgtgtgggttggaaccgaaga 1794
      .
1574 ttgttcattcgattaaagaca.....gtggtgcgttacctgcg 1611
      | | | | | | | | | | | | | | | | | |
1795 ttttctctttttttctgccacgagaggttctctggaggcatactctcca 1844
      .
1612 gttttggggagcttggttcgttggtgtgtgcaactggttggtacttctctgtt 1661
      | | | | | | | | | | | | | | | | | |
1845 gcaccgtgggctaataacgcgttggtccaattcagtcctggccttgcatgc 1894
      .
1662 cttcaaaggagctaataatTga..... 1683
      | | | | | | | | | | | | | | | | | |
1895 atgcaataaataaagtgatgggtttccctggtttcaat 1931

```

GAP (Present application SEQ ID NO 2 versus Duvich SEQ ID NO 2)

GAP of: Present application SEQ ID NO 2 from: 1 to: 560

readseq-64383_tmp_1 560 bp

to: DUVICK SEQ ID NO 2 from: 1 to: 566

readseq-34465_tmp_1 566 bp

Symbol comparison table: /applications/gcg/share/matrix/blosum62.cmp
CompCheck: 1102

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Quality:	1080	Length:	624
Ratio:	1.929	Gaps:	6
Percent Similarity:	52.988	Percent Identity:	44.024

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

x May 16, 2008 18:50 ..

```
1 .....MAHLQRTFPTMSKGRASFPGFLFGTASSSYQYEGAVNE 40
      .| .|. . | || | | |.|.|| ||| ||
51 FTTRSARVGSQNGVQMLSPSEIPQ.RDWFPDFTFGAATSAYQIEGAWNE 99
      .
41 GARGQSVWDHFSNRFPHRISDSSDGNVAVDFYHRYKEDIKRMKDINMDSF 90
      :|:| |||| . | || | |. .: . || || |: :|: . ||.:
100 DGKGESNWDHFCNHHPERILDGSNSDIGANSYHMYKTDVRLKEMGMDAY 149
      .
91 RLSIAWPRVLPYGKRDGRVSEEGIKFYNDVIDELLANEITPLVTIFHWDI 140
      | ||.||||:| | :| :| :|||:| ..|. || | | ||||| |:
150 RFSISWPRILPKGTKEGGINPDGIKYRNLINLLENGIEPYVTIFHWDV 199
      .
141 PQDLEDEYGGFLS...EQIIDDFRDYASLCFERFGDRVSLWCTMNEPWVY 187
      || ||:..|||| . |::: :| .||: |||:| | | ||| :
200 PQALEEKYGGFLDKSHKSIVEDYTYFAKVCFDNFGDKVKNWLTFNEPQTF 249
      .
188 SVAGYDTGRKAPGRCSKYVNGASVAGMSGYEAYIVSHNMLLAHAEAVEVF 237
      . | || ||||| .. | | | | |.|||||||:..
250 TSFSYGTGVFAPGRCSPLDCAYPGTGNSLVEPYTAGHNILLAHAEAVDLY 299
      .
238 RKCDHIKNGQIGIAHNPLWYEPYDPSDDVEGCNRAMDFMLGWHQHPTA 287
      | .|:| . : || | | : |. | ||| |
300 NKHYKRDDTRIGLAFDVMGRVPYGTSLDK.QAEERSWDINLGFLEPVV 348
      .
288 CGDYPETMKKSVGDRLPSTPEQSKKLIGSCDYVGINYSSLFVKSIAKHV 337
      |||| .|: :||| | || .|| || . .:|:| . | |. |
349 RGDYPFSMRSLARERLPFFKDEQEKLAGSYNMLGLNYTTSRFSKNIDIS 398
      .
338 DPTQPTWRITDQGVDMKTN.IDGKQIAKQGGSEWSFTYPTGLRNILKYVK 386
      | | | | . | || | | . | : | | | :.: | ..
```

```

399 PNYSPLNTDDAYASQEVNGPDGKPIGPPMGNPWIYMYPEGLKDLLMIMK 448
387 KTYGNPPILITENGYGEVAEQSQSLYMYNPSIDTERLEYIEGHIHAIHQ 436
      ||||| ||||| |:| . | | | .||:|: || : :.
449 NKYGNPPIYITENGIGDVDTKETPLPMEAALNDYKRLDYIQRHIATLKES 498
437 IHEDGVRVEGYVWSLLDNFEWNSGYGVRYGLYYIDYKDGLRRYPKMSAL 486
      | : | |:|: ||||| |. |: ||: |:| . || | |
499 I.DLGSNVQGYFAWSLLDNFEWFAGFTERYGIVYVDRNNNCTRYMKESAK 547
487 WLKEFLRFDQEDDSSTSKKEEKESYGKQLLHSVQDSQFVHSIKDSGALP 536
      ||||| .|. || ||
548 WLKEF.....NTAKKPSKILTPA..... 566

```

GAP of: Present application from: 1 to: 1683

to: DUVICK from: 1 to: 1931

Symbol comparison table: /applications/gcg/share/matrix/nwsgapdna.cmp
CompCheck: 8760

```
Match display thresholds for the alignment(s):
| = IDENTITY
: = 5
. = 1
```

```

1 .....atg 3
|
151 agcgaagggtttaaccttagctttacgccacgatctgcaagagttaggcaat 200
      .               .               .               .
4   gcacatcttcaaagaacatttcctactgagatgtcaaaaggtagagctag 53
    | | |           | | |         | | |       | | |     |
201 caaatggagtgccaattgttgagcccttcggaaatccctcgaagggactg 250
      .               .               .               .
54 ctttcctaaaaggctttctcttggaaactgcttcattcttcttatcagtacg 103
    | | |     | | |   | | | | | | | | | | | | | | | | |
251 gttcccctctgacttcattcttgggtgcgcgcacttcagcgctaccaaatg 300
      .               .               .               .
104 aaggagcagtgaatgaaggtgcbgaggacaaaagcgtgtgggatcatcttc 153
    | | | | | | | | | | | | | | | | | | | | | | | |
301 aaggtgcttggaaacgaagatggaaaggggaaagcaattgggatcacttc 350
      .               .               .               .
154 tccaacaggtttcctcacagaatcagtgattctagcgacggaaacgttgc 203
    | | | | | | | | | | | | | | | | | | | | | | |
351 tgccacaattttccggaaaggataatggacgggagcaatgcagacattgg 400
      .               .               .               .
204 cgttgatttctaccatcggttacaaaggaagatattaagagaatgaaggata 253
    | | | | | | | | | | | | | | | | | | | | | | |
401 agcgaattcgtaccatatgtacaaaacggatgtcagattgctgaaggaaa 450
      .               .               .               .
254 taaacatggattcggttcggttccattgcttggccacgagttctacct 303
    | | | | | | | | | | | | | | | | | | | | | | |
451 tgggcatggacgcataataggttctctatctcttggcctagaataactgcct 500
      .               .               .               .
304 tatggcaaaagggatagaggagttagtgaagaaggaattaagttttacaa 353
    | | | | | | | | | | | | | | | | | | | | | | |

```

501 aaggggaacgggtcgaaggaggtattaaccaggatggcatcgattactacaa 550
354 tgatgttattgatgaactcttagccaatgaaatcactcctcttggtacta 403
| | | | | | | | | | | | | | | | | | | | | |
551 aaggctcatcaacttggtgctagagaatggcatagagccatatgtaacaa 600
404 tctttcattgggacataaccacaggatccttgaagatgaatacggcgggtttt 453
| | | | | | | | | | | | | | | | | | | | | |
601 ttttccactgggatgtccctcaagcactagaagagaagtacggcgggattc 650
454 cta.....agcgagcagattatagatgacttcagagactatgcgag 494
| | | | | | | | | | | | | | | | | | | | | |
651 ttagataagactcagaagaggattgtaaatgattacaaaaacttcgctaa 700
495 tctctgcttcgagagatttggggacagagtgaagtctgtggtgcacaatga 544
| | | | | | | | | | | | | | | | | | | | | |
701 ggtgtgcttcgacaacttgggtgacaagggtgaagaattggttgaccttta 750
545 atgagccgtgggtctacagtgtcgcggttatgacacaggaaggaaagcg 594
| | | | | | | | | | | | | | | | | | | | | |
751 atgagccccagacatttacttcattttcctatggaaccgggtctttgcc 800
595 ccaggacggtgctccaagtatgttaatggcgctagtgttgctggaatgtc 644
| | | | | | | | | | | | | | | | | | | | | |
801 ccaggacgatgctcaccgggactagactgtgccatcccaactgggaattc 850
645 gggatacgaggcatatattgtgagccataacatgcttctagcgcacgcag 694
| | | | | | | | | | | | | | | | | | | | | |
851 actcgtcgaaccttacattgctggccacaacattcttctagcccacgctg 900
695 aagcagtgggaagtgtttagaaaatgtgaccatattaaaaacggacaaatt 744
| | | | | | | | | | | | | | | | | | | | | |
901 aggctgttgatctttacaacaagtattacaagggcgagaacggccgcata 950
745 gggattgcgcataatccactttggtacgagccatatgatccgagtgatcc 794
| | | | | | | | | | | | | | | | | | | | | |
951 ggtcttgcatTTgatgtaatgggtcgtgtgccatacggaacatcatttct 1000
795 agatgatgtcgaaggatgtaatcgagctatggacttcagtcttggttggc 844
| | | | | | | | | | | | | | | | | | | | | |
1001 agatga...acaggccaaagaaagggtccatggacattaacctaggatggt 1047
845 atcagcatccgactgcttgtggagactatccagaaacgatgaagaaatca 894
| | | | | | | | | | | | | | | | | | | | | |
1048 tcttgagcctgtggttcgtggtgactacccttctcaatgagatcgтта 1097
895 gttggagatagattaccgagttttacaccagaacaatctaagaaacttat 944
| | | | | | | | | | | | | | | | | | | | | |
1098 gcgaggggaacgactacccttcttcagtgacaaacagcaagagaagcttgt 1147
945 aggctcttgcgattacgttggtataaaactactatagctcgcttttctgta 994
| | | | | | | | | | | | | | | | | | | | | |
1148 gggatcctataacatggtgggaataaaactactacacctcaatattctcca 1197
995 agagtatcaaacacgtggatcctacgcaacctacttggaactgaccaa 1044
| | | | | | | | | | | | | | | | | | | | | |
1198 aacatatcgacatctcaccaaaatactcgctgttctcaacactgacgac 1247
1045 ggcgttgattggatgaaaaccaa...catagatgggaaacaaatagcaaa 1091
| | | | | | | | | | | | | | | | | | | | | |
1248 gcctacgctagtcaagaaacgtatgggcctgacgggaaaccattgggtcc 1297
1092 acaaggaggatcagagtggagttttcacatatccaacaggactcagaaaca 1141

```

      | | | | | | | | | | | | | | | | | |
1298 tcctatgggaaatccgtggatctacttataccagaaggcctaaaggata 1347
      | | | | | | | | | | | | | | | | | |
1142 ttttgaagtatgtgaaaaaaacttatggcaatcctccattctcataact 1191
      | | | | | | | | | | | | | | | | | |
1348 tccttatgatcatgaagaacaaatatggaaacccacctatctacatcact 1397
      | | | | | | | | | | | | | | | | | |
1192 gaaaacgggtatggtgaagtagcggaacagagtcagagtcctttatatatga 1241
      | | | | | | | | | | | | | | | | | |
1398 gagaacggaatcggggatggtgatacaaaggagaaacctctacccatgga 1447
      | | | | | | | | | | | | | | | | | |
1242 caatccttcaatcgacacagagagattggagtacattgaaggacatatcc 1291
      | | | | | | | | | | | | | | | | | |
1448 ggctgccttaaataactacaaaaggctagattacatccagcgccacatct 1497
      | | | | | | | | | | | | | | | | | |
1292 acgctattcatcaagccatccatgaagatggagtaagagtggaagggttat 1341
      | | | | | | | | | | | | | | | | | |
1498 caactctcaaggagtcaat...agacttgggagcaaatgtgcatgggtac 1544
      | | | | | | | | | | | | | | | | | |
1342 tacgtatggtcattgctagataacttcgagtggaaacagtggatatggtgt 1391
      | | | | | | | | | | | | | | | | | |
1545 ttcgcttggtctctgctggataactttgaatggtacgccggctacaccga 1594
      | | | | | | | | | | | | | | | | | |
1392 gagatatggtttatattacattgattacaaagatgggcttagacgataacc 1441
      | | | | | | | | | | | | | | | | | |
1595 acgttatggcattgtctacgtcgaccgcacaaaataactacacgcgctaca 1644
      | | | | | | | | | | | | | | | | | |
1442 cgaaaatgtcggcggttatggttgaaagagttcttga.....ggtttg 1483
      | | | | | | | | | | | | | | | | | |
1645 tgaaggagtcagccaagtggttaaaagagttcaatactgcgaagaagcct 1694
      | | | | | | | | | | | | | | | | | |
1484 atcaagaagacgattcttcgacgtctaagaaagaaga..... 1520
      | | | | | | | | | | | | | | | | | |
1695 agcaagaagattattacgccagcttaaaaacatgggacctcgtgatgtgg 1744
      | | | | | | | | | | | | | | | | | |
1521 gaagaaagagagctatggaaaacagttattgcattctgttcaggacagtc 1570
      | | | | | | | | | | | | | | | | | |
1745 gtacggtgccacccatgaaataaaaacctagtgtgtggtttgaaacctaa 1794
      | | | | | | | | | | | | | | | | | |
1571 aatttggttcattcgattaaagacagtg...gtgcgttacctgcggttttg 1617
      | | | | | | | | | | | | | | | | | |
1795 atttttctttttcttttttgcacccatgagagaggtagtggagtcatttc 1844
      | | | | | | | | | | | | | | | | | |
1618 gggagcttggtcggtgtgtctgcaactgttggtacttctctgttcttcaa 1667
      | | | | | | | | | | | | | | | | | |
1845 tccagcaccgtggctaataatgtattgttgagtacaatctagcattgtc 1894
      | | | | | | | | | | | | | | | | | |
1668 aggagctaataatTga..... 1683
      | | | | | | | | | | | | | | | | | |
1895 gtcatgcaataaataaagtgactggtttccctatttc 1931

```

GAP (Present Application SEQ ID NO 2 versus Duvick SEQ ID NO 4)

GAP of: Present Application from: 1 to: 560

readseq-8408_tmp_1 560 bp

to: DUVICK from: 1 to: 563

readseq-6249_tmp_1 563 bp

Symbol comparison table: /applications/gcg/share/matrix/blosum62.cmp
CompCheck: 1102

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Quality:	1138	Length:	621
Ratio:	2.032	Gaps:	6
Percent Similarity:	54.582	Percent Identity:	45.418

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

x May 16, 2008 18:54 ..

```
1 .....MAHLQRTFPTMSKGRASFPGKFLFGTASSSYQYEGAVNEGAR 43
      .| .|. .: | || |:| |.|. | || | | :
51 RSARVGNQNGVQLLSPSEIPR.RDWFPSPDFIFGAATSAYQIEGAWNEDGK 99
      .
44 GQSVWDHFSNRFPHRISDSSDGNVAVDFYHRYKEDIKRMKDINMDSFRLS 93
      |:| |||| . || || | . .: . || || |:| :|:. ||:| |
100 GESNWDHFCNFPERIMDGSNADIGANSYHMYKTDVRLLEKMGMDAYRFS 149
      .
94 IAWPRVLPYGKRDGRGVSEEGIKFYNDVIDELLANEITPLVTIFHWDIPQD 143
      |.|||:| | : |:|:| | : |. || | | | |||||:| |
150 ISWPRILPKGTVEGGINQDGIDYYKRLINLLENGIEPYVTIFHWDVPQA 199
      ||:| |||| ..|:|:|:| |. |:| |||:| | | || | :.
200 LEEKYGGFLDKTQKRIVNDYKNFAKVCFDNFGDKVKNWLTfNEPQTFTSF 249
      .
191 GYDTGRKAPGRCSKYVNGASVAGMSGYEAYIVSHNMLLAHAEAVEVFRKC 240
      | || | |||| | .. | | | | | | |. |||||:|:| |
250 SYGTGVFAPGRCSPLDCAIPTGNSLVEPYIAGHNILLAHAEAVDLYNKY 299
      .
241 DHIKNGQIGIAHNPLWYEPYDPSDDVEGCNRAMDFMLGWHQHPTACGD 290
      .||:|:| . : || | |:| .|. | || | | | |
300 YKGENGRIGLAFDVMGRVPYGTSLFDE.QAKERSMDINLGWFLEPVVRGD 348
      .
291 YPETMKKSVGDRLPSTPEQSKKLIGSCDYVGINYYSSLFVKSIIKHVDPT 340
      || .: :||| |. . | |:| |. . |||||:| | |
349 YPFMSRSLARERLPFFSDKQKEKLVGSYNMLGINYYTSIFSIIKHIDISPKY 398
      .
341 QPTWRDQGVDMKT.NIDGKQIAKQGGSEWSFTYPTGLRNILKYVKKTY 389
      .| || | | | | |. | : | | |:| | | |
```



```

399 SPVLNTDDAYASQETYGPDGKPIGPPMGNPWIYLYPEGLKDILMIMKNKY 448
390 GNPPILITENGYGEVAEQSQSLYMYNPSIDTERLEYIEGHIHAIHQAIHE 439
    ||||| ||||| |:| . . | | | .||:|:| | | : :. | :
449 GNPPIYITENGIGDVDTKKPLPMEALNDYKRLDYIQRHISTLKESI.D 497
440 DGVRVEGYVWSLLDNFEWNSGYGVRYGLYYIDYKDGLRRYPKMSALWLK 489
    | | |:| ||||| | | .|| | |:| |:| | . | | | | |
498 LGANVHGYFAWSLLDNFEWYAGYTERYGIVYVDRKNKYTRYMKESAKWLK 547
490 EFLRFDQEDDSSTSKKEEKESYGKQLLHSVQDSQFVHSIKDSGALPAVL 539
    || .|.|| | |
548 EF.....NTAKKPSKKIITPA..... 563

```

BestFit (Present Application SEQ ID NO 1 versus Duvick SEQ ID NO 1)

BESTFIT of: Present Application from: 1 to: 1683

readseq-5573_tmp_1 1683 bp

to: DUVICK from: 1 to: 1931

readseq-46685_tmp_1 1931 bp

Symbol comparison table: /applications/gcg/share/matrix/swgapdna.cmp
CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	1138	Length:	1437
Ratio:	0.807	Gaps:	12
Percent Similarity:	54.500	Percent Identity:	54.500

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

28084.seq1.fas x 28084.seq2.fas May 16, 2008 19:01 ..

```
64 ggctttctctttggaactgcttcatcttcttatcagtacgaaggagcagt 113
   ||| ||| || | || | || | ||| |||
272 gacttcaccttcggtgccgaccttcagcgtaacaaattgaagggtgcttg 321
   ||| ||| ||| ||| ||| ||| ||| ||| |||
114 gaatgaagggtgcgagaggacaaagcgtgtgggatcatttctccaacaggt 163
   ||| ||| ||| ||| ||| ||| ||| ||| |||
322 gaatgaagatggaaagggggaagcaactgggatcacttctgccacaatc 371
   ||| ||| ||| ||| ||| ||| ||| ||| |||
164 ttcttcacagaatcagtgattctagcgacggaacgttgccgttgatttc 213
   ||| ||| ||| ||| ||| ||| ||| ||| |||
372 atccggaaggatactggacgggagcaattcagacattggagcgaattcg 421
   ||| ||| ||| ||| ||| ||| ||| ||| |||
214 taccatcggttacaaggaagatattaagagaatgaaggatataaacatgga 263
   ||| ||| ||| ||| ||| ||| ||| ||| |||
422 tatcatatgtacaaaacggacgtcagattgctcaaggaaatgggcatgga 471
   ||| ||| ||| ||| ||| ||| ||| ||| |||
264 ttcgttttcggtttccattgcttggecacgagttctaccttatggcaaaa 313
   ||| ||| ||| ||| ||| ||| ||| ||| |||
472 cgcatataggttctctatctcttgcccagaatactgccgaagggaacca 521
   ||| ||| ||| ||| ||| ||| ||| ||| |||
314 gggatagaggaggttagtgaagaaggaattaagttttacaatgatgttatt 363
   ||| ||| ||| ||| ||| ||| ||| ||| |||
522 aagaaggaggtattaaccctgatggcatcaagtactacagaaacctcatc 571
   ||| ||| ||| ||| ||| ||| ||| ||| |||
364 gatgaactcttagccaatgaaatcactcctcttggttactatctttcattg 413
   ||| ||| ||| ||| ||| ||| ||| ||| |||
572 aacttggtgctggaaaacggcatagagccatatgtaacaattttccactg 621
   ||| ||| ||| ||| ||| ||| ||| ||| |||
414 ggacataccacaggatcttgaagatgaatacggcggttttc....taagc 459
   ||| ||| ||| ||| ||| ||| ||| ||| |||
622 ggatgtacctcaagcactagaagagaagtacggcggttccttagataaga 671
   ||| ||| ||| ||| ||| ||| ||| ||| |||
460 g.....agcagattatagatgacttcagagactatgcgagtctctgcttc 504
```

672 gtcataagagcattgtagaagattacacacttctcgctaagggtgtgcttt 721
 505 gagagatttggggacagagtgagtcgtgtggtgcacaaatgaatgagccgtg 554
 722 gataacttcggcgacaaggatgaagaattgggtgacctttaatgagcccca 771
 555 ggtctacagtgtcgcgggctatgacacaggaaggaaagcgcaggacggg 604
 772 gacatttacttccttttctacggaactggggctcttgccccagggtcggt 821
 605 gctccaagtatgttaatggcgctagtgttgctggaatgtcgggatacag 654
 822 gctcacctggactagactgtgcctaccaactgggaattcactcgtcgag 871
 655 gcataatattgtgagccataacatgcttctagcgcacgcagaagcagtgga 704
 872 ccttacactgctggccataacattctcctagcccacgctgaggtgttga 921
 705 agtgtttagaaaatgtgaccatattaaaaacggacaaattgggattgcgc 754
 922 tctttacaacaagcattacaagcgcgacgacacccgcatagggcttgct 971
 755 ataatccacttttggtacgagccatgatccgagtgatccagat...gat 801
 972 ttgacgtaaatgggtcgtgtgccatacgggaacatcgtttctggataaacag 1021
 802 gtcgaaggatgtaatcgagctatggacttcatgcttggttgcatcagca 851
 1022 gccgaag.....aaaggatcatgggacatcaacctaggatggttcttaga 1065
 852 tccgactgcttgtggagactatccagaaacgatgaagaaatcagttggag 901
 1066 gccagtggttcgtgggtgactacccttctccatgagatcattggctaggg 1115
 902 atagattaccgagttttacaccagaacaatctaagaaacttataggctct 951
 1116 aacgactacccttcttcaaggacgagcagaaggagaagctcgcgggttcc 1165
 952 tgcgattacggttggtataaaactactatagctcgcttttctgtaagagtat 1001
 1166 tataacatgttgggttaaactactacacctcacggttctccaa..... 1209
 1002 caaacacgtggatcctacgcaacctact.....tggagaactgacca 1043
 1210 .aaacatcgacatctcac.caaactactcacctgtgctcaacactgacga 1257
 1044 aggcgttgattg....gatgaaaaccaacatagatgggaaacaaatagca 1089
 1258 cgcctacgccagtcaagaagttaacgggcct.gacgggaagcccattggt 1306
 1090 aaacaaggaggatcagagtggtgtttcacatatccaacaggactcagaaa 1139
 1307 cctcctatgggaaatccatggatctacatgtaccctgagggcttgaagga 1356
 1140 cattttgaagtatgtgaaaaaaacttatggcaatcctcccattctcataa 1189
 1357 tctccttatgataatgaagaacaaatacggaaaccacctatctacatca 1406
 1190 ctgaaaacgggtatggtgaagtag...cggaacagagtcagagtcctttat 1236
 1407 ccgagaacggaatcggggatgttgataccaaagagacac...ctctaccc 1453

```

1237 atgtacaatccttcaatcgacacagagagattggagtacattgaaggaca 1286
    ||| | | | | | | | | | | | | | | | | | | |
1454 atggaggctgccttaaatagactacaaaaggctagattacatccagcgcca 1503
    .
1287 tatccacgctattcatcaagccatccatgaagatggagtaagagtggaag 1336
    ||| | | | | | | | | | | | | | | | | |
1504 catcgctactcttaaggaaatcaat...agacttgggatcaaatgtgcaag 1550
    .
1337 gttattacgtatgggtcattgctagataaacttcgagtggaacagtggatat 1386
    | | | | | | | | | | | | | | | | | | |
1551 gctacttcgcttggtctctgctggacaactttgaatggtttgccggcttc 1600
    .
1387 ggtgtgagatatggtttatattacattgattacaaagatgggcttagacg 1436
    | | | | | | | | | | | | | | | | | |
1601 accgaacgttatggcattgtctacgtcgaccgcaacaataactgcacgcg 1650
    .
1437 atacccgaaaatgtcggcggttatggttgaaagagttc 1473
    ||| ||| ||| || | ||||| ||||| |||
1651 ctacatgaaggagtctgccaaagtggttgaaagagttc 1687

```

BESTFIT of: Present Application from: 1 to: 560

to: DUVICK from: 1 to: 566

Symbol comparison table: /applications/gcg/share/matrix/blosum62.cmp
CompCheck: 1102

Quality:	1094	Length:	492
Ratio:	2.242	Gaps:	5
Percent Similarity:	53.814	Percent Identity:	44.536

```
1 = IDENTITY
: = 2
= 1
```

[illegible]

462 GIGDVDTKETPLPMEALNDYKRLDYIQRHIATLKESI.DLGSNVQGYFA 510

450 WSLLDNFEWNSGYGVRYGLYYIDYKDGLRRYPKMSALWLKEF 491

|||||||. |: ||: |:| . || || |||||

511 WSLLDNFEWFAGFTERYGIVYVDRNNNCTRYMKESAKWLKEF 552

BestFit (Present Application SEQ ID NO 1 versus Duvick SEQ ID NO 3)

BESTFIT of: Present Application from: 1 to: 1683

readseq-56847_tmp_1 1683 bp

to: DUVICK from: 1 to: 1931

readseq-29531_tmp_1 1931 bp

Symbol comparison table: /applications/gcg/share/matrix/swgapdna.cmp

CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000

Quality:	1782	Length:	1433
Ratio:	1.264	Gaps:	8
Percent Similarity:	56.066	Percent Identity:	56.066

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

. = 1

30007.seq1.fas x 30007.seq2.fas May 16, 2008 19:04 ..

```

      .
      .
      .
64  ggctttctctttggaactgcttcatcttcttatcagtacgaaggagcagt 113
    ||| ||||| | || | || | ||| || ||||| ||
261  gacttcatctttggtgccgaccttcagcgtaccaaattgaagggtgcttg 310
      .
114  gaatgaagggtgcgagaggacaaagcgtgtgggatcatttctccaacaggt 163
    || |||| | | |||| | ||||| ||||| |||| |
311  gaacgaagatggaaaggggaaagcaattgggatcacttctgccacaatt 360
      .
164  ttcctcacagaatcagtgattctagcgacggaaacggttgccgttgatttc 213
    |||| | || || | || |||| | || |||| | |||
361  ttccgaaaaggataatggacgggagcaatgcagacattggagcgaattcg 410
      .
214  taccatcggttacaaggaagatattaagagaatgaaggatataaacatgga 263
    ||||| |||| | || | | ||||| || |||||
411  taccatatgtacaaaacggatgtcagattgctgaaggaaatgggcatgga 460
      .
264  ttcgttttcggctttccattgcttggccacgagttctaccttatggcaaaa 313
    | | | || | || | ||||| || | || | || |
461  cgcatataggttctctatctcttggcctagaatactgcctaagggaacgg 510
      .
314  gggatagaggagttagtgaagaaggaattaagttttacaatgatgttatt 363
    || |||| ||| | || || | || | |||| | ||
511  tcgaaggaggtattaaccaggatggcatcgattactacaaaaggctcatc 560
      .
364  gatgaactcttagccaatgaaatcactcctcttggttactatctttcattg 413
    | | | || |||| || || |||| | || |||| |
561  aacttggttgctagagaatggcatagagccatatgtaacaattttccactg 610
      .
414  ggacataccacaggatcttgaagatgaatacggcggttttcta..... 456
    ||| | || || | || |||| | ||||| || ||
611  ggatgtccctcaagcactagaagagaagtacggcggattcttagataaga 660
      .
457  ..agcgagcagattatagatgacttcagagactatgcgagtctctgcttc 504
```

```

      || ||||| || ||||| || || ||||| || || |||||
661 ctcagaagaggattgtaaatgattacaaaaacttcgctaagggtgtgcttc 710
505 gagagatttggggacagagtgagtcgtggtgcacaaatgaatgagccgtg 554
      || | ||||| ||||| ||||| ||||| || || |||||
711 gacaactttggtgacaagggaagaattggttgaccttaatgagcccca 760
555 ggtctacagtgtcgcgggctatgacacaggaaggaaagcggcaggacggt 604
      | | | | | ||||| ||||| || |||||
761 gacatttacttcattttcctatggaaccgggggtctttgcccaggacgat 810
605 gctccaagtatgttaatggcgctagtgttgctggaatgtcgggatacag 654
      ||||| | | | | | ||||| || || |||||
811 gctcaccgggactagactgtgccatcccaactgggaattcactcgtcgaa 860
655 gcataatattgtgagccataacatgcttctagcgcacgcagaagcagtgga 704
      | || ||||| ||||| ||||| ||||| ||||| || |||||
861 ccttacattgctggccacaacattcttctagcccacgctgaggtgttga 910
705 agtgtttagaaaaatgtgaccatattaaaaacggacaaattgggattgcg 754
      | | | | | ||||| || || ||||| || || |||||
911 tctttacaacaagtattacaagggcgagaacggccgcataaggtcttgc 960
755 ataatccactttggtacgagccatatgatccgagtgatccagatg...at 801
      | || | | | | ||||| || || ||||| || || |||||
961 ttgatgtaaatgggtcgtgtgccatacggaaacatcatttctagatgaacag 1010
802 gtcgaaggatgtaatcgagctatggacttcatgcttggttggcatcagca 851
      | | ||||| ||||| ||||| || || |||||
1011 gccaaag.....aaagggtccatggacattaacctaggatggttcttgg 1054
852 tccgactgcttgtggagactatccagaaacgatgaagaaatcagttggag 901
      || | | ||||| ||||| || ||||| || || |||||
1055 gcctgtggttcgtggtgactacccttctcaatgagatcgttagcgaggg 1104
902 atagattaccgagttttacaccagaacaatctaagaaacttataggtct 951
      | || ||||| || || ||||| ||||| ||||| || |||||
1105 aacgactacccttcttcagtgacaaacagcaagagaagcttgtgggatcc 1154
952 tgcgattacggttggtataaaactactatagctcgcttttctggaagagtat 1001
      | | | | ||||| ||||| ||||| || || |||||
1155 tataacatggttgggaataaaactactacacctcaatattctccaaacatat 1204
1002 caaacacgtggatcctacgcaa.....cctacttggagaactgaccaa 1044
      || | ||||| ||||| || ||||| || || |||||
1205 cga.....catctcaccaaaatactcgctgttctcaacactgacgac 1247
1045 ggcgttgattggatgaaaaccaa...catagatgggaaacaaatagcaaa 1091
      || | | | | ||||| || || ||||| || || |||||
1248 gcctacgctagtcaagaaacgtatgggcctgacgggaaacccattggtcc 1297
1092 acaaggaggatcagagtggagtttcacatatccaacaggactcagaaaca 1141
      | ||||| ||||| || ||||| ||||| ||||| || |||||
1298 tcctatgggaaatccgtggatctacttataccagaaggcctaaaggata 1347
1142 ttttgaagtatgtgaaaaaaacttatggcaatcctcccattctcataact 1191
      ||||| || ||||| ||||| ||||| ||||| ||||| |||||
1348 tccttatgatcatgaagaacaaatatggaaaccacctatctacatcact 1397
1192 gaaaacgggtatggtgaagtagcggaacagagtcagagtctttatatgta 1241
      || ||||| || || ||||| || || ||||| || || |||||
1398 gagaacggaatcggggatgttgatacaaaggagaaacctctacccatgga 1447

```



```

1242 caatccttcaatcgacacagagagattggagtacattgaaggacatatcc 1291
    | | | | | | | | | | | | | | | | | | | | | |
1448 ggctgccttaaatagactacaaaaggctagattacatccagcgccacatct 1497
    .
1292 acgctattcatcaagccatccat.gaagatggagtaagagtggaaggtta 1340
    | | | | | | | | | | | | | | | | | | | | | |
1498 caact....ctcaaggagtcaatagacttgggagcaaagtgcacatggcta 1543
    .
1341 ttacgtatggtcattgctagataaacttcgagtgggaacagtggatatggtg 1390
    | | | | | | | | | | | | | | | | | | | | | |
1544 cttegcttgggtctctgctggataaactttgaatggtagcgccggctacaccg 1593
    .
1391 tgagatatgggtttatattacattgattacaaagatgggcttagacgatac 1440
    | | | | | | | | | | | | | | | | | | | | | |
1594 aacgttatggcattgtctacgtcgaccgcaaaaataactacacgcgctac 1643
    .
1441 ccgaaaatgtcggcggttatggttgaaagagttc 1473
    | | | | | | | | | | | | | | | | | | | | | |
1644 atgaaggagtcagccaagtgggttaaaagagttc 1676

```

BestFit (Present Application SEQ ID NO 2 versus Duvick SEQ ID NO 4)

BESTFIT of: Present Application from: 1 to: 560

readseq-44782_tmp_1 560 bp

to: DUVICK from: 1 to: 563

readseq-7768_tmp_1 563 bp

Symbol comparison table: /applications/gcg/share/matrix/blosum62.cmp
CompCheck: 1102

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248

Quality:	1152	Length:	492
Ratio:	2.361	Gaps:	5
Percent Similarity:	55.464	Percent Identity:	45.979

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

26267.seq1.fas x 26267.seq2.fas May 16, 2008 18:58 ..

```

      4 LQRTFPTMSKGRASFPKGFLFGTASSSYQYEGAVNEGARGQSVWDHFSN 53
      .|  .|. : |  ||  |:||  |.|.||  |||  ||  :|:|  ||||  .
    61 VQLLSPSEIPR.RDWFPSPDFIFGAATSAYQIEGAWNEDGKGESNWDHFCH 109

    54 RFPHRISDSSDGNVAVDIFYHRYKEDIKRMKDINMDSFRLSIAPRVLPGY 103
      ||  ||  |.  .:  .  ||  ||  |:  |:  |:  |:  |:  |:  |:  |
   110 NFPERIMDGSNADIGANSYHMYKTDVRLKEMGMDAYRFSISWPRILPKG 159

   104 KRDRGVSEEGIKFYNDVIDELLANEITPLVTIFHWDIPQDLEDEYGGFL. 152
      :  |:  |:  |:  |:  |.  ||  ||  ||  ||  ||  ||  ||  |:  |:  |
   160 TVEGGINQDGDIDYKRLINLLLENGIEPYVTIFHWDVPQALEEKYGGFLD 209

   153 ..SEIIDDFRDYASLCFERFGDRVSLWCTMNEPWVYSVAGYDTGRKAPG 200
      ..|:  |:  |:  |:  |  |:  |:  |:  |:  |  ||  ||  ||  |:  |
   210 KTQKRIVNDYKNFAKVCDFNFGDKVKNWLTFNEPQTFSTFSYGTGVFAPG 259

   201 RCSKYVNGASVAGMSGYEAYIVSHNMLLAHAEAVEVFRKCDHIKNGQIGI 250
      |||  ..  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   260 RCSPGLDCAIPTGNSLVEPYIAGHNILLAHAEAVDLYNKYYKGENGRIGL 309

   251 AHNPLWYEPYDPSDPDDVEGCNRAMDFMLGWHQHPTACGDYPETMKKSVG 300
      |  .  :  ||  |  |:  :  |.  ||  |||  |  ||||  .|:
   310 AFDVMGRVPYGTSLDE.QAKERSMDINLGFLEPVVRGDYPFSMRSLAR 358

   301 DRLPSTPEQSKKLIGSCDYVGINYSSLFVKSIXHVDPTQPTWRTDQGV 350
      :|||  |.  .|  .|:  |:  |.  .|  ||||  |:  |  |  |  |
   359 ERLPFFSDKQQEKLVGSYNMLGINYYTSIFS KHIDISPKYSPVLNTDDAY 408

   351 DWMKT.NIDGKQIAKQGGSEWSFTYPTGLRNILKYVKKTYGNPPILITEN 399
      .|  |||  |  |.  |  :  ||  |:  .|  |  ||||  ||||
   409 ASQETYGPDGKPIGPPMGNPWIIYLYPEGLKDILMIMKNKYGNPPIYITEN 458

   400 GYGEVABEQSQSLYMYNPSIDTERLEYIEGHIHAIHQAIHEDGVRVEGYV 449
      |  |:  |.  .|  |  |  |  |  |  |  |  |  |  |  |  |  |
```

459 GIGDVDTKKPLPMEALNDYKRLDYIQRHISTLKESI.DLGANVHGYFA 507

450 WSLLDNFEWNSGYGVRYGLYYIDYKDGLRRYPKMSALWLKEF 491

||||||| .|| |||: |:| |. || | || |||

508 WSLLDNFEWYAGYTERYGIVYVDRKNNYTRYMKESAKWLKEF 549